



SEQUENCE LISTING

<110> Carulli, John P.
Little, Randall D.
Recker, Robert R.
Johnson, Mark L.

<120> High bone mass gene of 11q13.3

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<140> US 09/543,771

<141> 2000-04-05

<150> US 09/229,319

<151> 1999-01-13

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Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
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Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg
335 340 345
acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc
1165
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
350 355 360 365
gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac
1213
Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp
370 375 380
ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc
1261
Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile
385 390 395
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1309
Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr
400 405 410
gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac
1357
Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn
415 420 425
ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc
1405
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu

430	435	440	445
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1453			
Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro			
450	455	460	
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac			
1501			
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp			
465	470	475	
tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag			
1549			
Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu			
480	485	490	
cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc			
1597			
Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala			
495	500	505	
ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac			
1645			
Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp			
510	515	520	525
aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg			
1693			
Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu			
530	535	540	
gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc			
1741			
Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe			
545	550	555	
atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag			
1789			
Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys			
560	565	570	
gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg			
1837			
Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met			
575	580	585	
ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt			
1885			
Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys			
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gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac			
1933			
Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His			
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gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg			
1981			
Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met			
625	630	635	
aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc			
2029			
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala			
640	645	650	
gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc			
2077			
Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile			
655	660	665	

ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc
2125
Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser
670 675 680 685
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2173
Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg
690 695 700
gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt
2221
Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu
705 710 715
gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac
2269
Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr
720 725 730
tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cggt gac ggg
2317
Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly
735 740 745
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2365
Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser
750 755 760 765
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Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly
770 775 780
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2461
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785 790 795
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2509
Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr
800 805 810
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2557
Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu
815 820 825
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Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu
830 835 840 845
ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca
2653
Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr
850 855 860
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2701
Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg
865 870 875
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2749
Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu
880 885 890
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2797
Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn
895 900 905
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Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg
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2893
Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys
930 935 940
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2941
Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser
945 950 955
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Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu
960 965 970
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3037
His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys
975 980 985
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3181
Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr
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Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu
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3997
Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln
1295 1300 1305
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	Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr		
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	Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro		
1375	1380	1385	
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	Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe		
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	Val Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro		
	1410	1415	1420
4381	ttc ccg cac gag tat gtc agc ggg acc ccg cac gtg ccc ctc aat ttc		
	Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe		
	1425	1430	1435
4429	ata gcc ccg ggc ggt tcc cag cat ggc ccc ttc aca ggc atc gca tgc		
	Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys		
	1440	1445	1450
4477	gga aag tcc atg atg agc tcc gtg agc ctg atg ggg ggc cgg ggc ggg		
	Gly Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly		
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4525	gtg ccc ctc tac gac cgg aac cac gtc aca ggg gcc tcg tcc agc agc		
	Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser		
1470	1475	1480	1485
4573	tcg tcc agc acg aag gcc acg ctg tac ccg ccg atc ctg aac ccg ccg		
	Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro		
	1490	1495	1500
4621	ccc tcc ccg gcc acg gac ccc tcc ctg tac aac atg gac atg ttc tac		
	Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr		
	1505	1510	1515
4669	tct tca aac att ccg gcc act gcg aga ccg tac agg ccc tac atc att		
	Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile		
	1520	1525	1530
4717	cga gga atg gcg ccc ccg acg acg ccc tgc agc acc gac gtg tgt gac		
	Arg Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp		
	1535	1540	1545
4765	agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat		
	Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp		
1550	1555	1560	1565
4813	ttg aac tcg gac tca gac ccc tat cca ccc cca ccc acg ccc cac agc		
	Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Thr Pro His Ser		
	1570	1575	1580

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 Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu
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 Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Ser Pro Cys Thr Asp
 1600 1605 1610
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 Ser Ser
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 35 40 45
 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
 50 55 60
 Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
 65 70 75 80
 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
 85 90 95
 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
 100 105 110
 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
 115 120 125
 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
 130 135 140
 Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
 145 150 155 160
 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
 165 170 175
 Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
 180 185 190
 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
 195 200 205
 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
 210 215 220
 Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
 225 230 235 240
 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
 245 250 255

Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys
260 265 270
Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser
275 280 285
Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
290 295 300
Gly Trp Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr
305 310 315 320
Cys Ala Cys Pro Thr Gly Val Gln Met Gln Asp Asn Gly Arg Thr Cys
325 330 335
Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg Thr Asp Leu
340 345 350
Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln
355 360 365
Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
370 375 380
Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala
385 390 395 400
Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn
405 410 415
Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp
420 425 430
Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr
435 440 445
Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
450 455 460
Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu
465 470 475 480
Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val
485 490 495
Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu
500 505 510
Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
515 520 525
Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
530 535 540
Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp
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Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala
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Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
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Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
595 600 605
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Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
625 630 635 640
Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His
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Arg Ile Ser Leu Glu Thr Asn Asn Asp Val Ala Ile Pro Leu Thr
660 665 670
Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His
675 680 685
Ile Tyr Trp Thr Asp Val Ser Leu Lys Asn Ile Ser Arg Ala Phe Met
690 695 700
Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro

705	710	715	720												
Glu	Gly	Met	Ala	Val	Asp	Trp	Met	Gly	Lys	Asn	Leu	Tyr	Trp	Ala	Asp
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Thr	Gly	Thr	Asn	Arg	Ile	Glu	Val	Ala	Arg	Leu	Asp	Gly	Gln	Phe	Arg
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Gln	Val	Leu	Val	Trp	Arg	Asp	Leu	Asp	Asn	Pro	Arg	Ser	Leu	Ala	Leu
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Asp	Pro	Thr	Lys	Gly	Tyr	Ile	Tyr	Trp	Thr	Glu	Trp	Gly	Gly	Lys	Pro
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Arg	Ile	Val	Arg	Ala	Phe	Met	Asp	Gly	Thr	Asn	Cys	Met	Thr	Leu	Val
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Asp	Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	Ala	Asp	Gln
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Arg	Leu	Tyr	Trp	Thr	Asp	Leu	Asp	Thr	Asn	Met	Ile	Glu	Ser	Ser	Asn
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Met	Leu	Gly	Gln	Glu	Arg	Val	Val	Ile	Ala	Asp	Asp	Leu	Pro	His	Pro
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Phe	Gly	Leu	Thr	Gln	Tyr	Ser	Asp	Tyr	Ile	Tyr	Trp	Thr	Asp	Trp	Asn
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Leu	His	Ser	Ile	Glu	Arg	Ala	Asp	Lys	Thr	Ser	Gly	Arg	Asn	Arg	Thr
							865					870			880
Leu	Ile	Gln	Gly	His	Leu	Asp	Phe	Val	Met	Asp	Ile	Leu	Val	Phe	His
							885					890			895
Ser	Ser	Arg	Gln	Asp	Gly	Leu	Asn	Asp	Cys	Met	His	Asn	Asn	Gly	Gln
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Cys	Gly	Gln	Leu	Cys	Leu	Ala	Ile	Pro	Gly	Gly	His	Arg	Cys	Gly	Cys
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Ala	Ser	His	Tyr	Thr	Leu	Asp	Pro	Ser	Ser	Arg	Asn	Cys	Ser	Pro	Pro
							930					935			940
Thr	Thr	Phe	Leu	Leu	Phe	Ser	Gln	Lys	Ser	Ala	Ile	Ser	Arg	Met	Ile
							945					950			960
Pro	Asp	Asp	Gln	His	Ser	Pro	Asp	Leu	Ile	Leu	Pro	Leu	His	Gly	Leu
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Arg	Asn	Val	Lys	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Asp	Lys	Phe	Ile	Tyr
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Trp	Val	Asp	Gly	Arg	Gln	Asn	Ile	Lys	Arg	Ala	Lys	Asp	Asp	Gly	Thr
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Gln	Pro	Phe	Val	Leu	Thr	Ser	Leu	Ser	Gln	Gly	Gln	Asn	Pro	Asp	Arg
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Ala	Met	Gly	Val	Val	Leu	Arg	Gly	Asp	Arg	Asp	Lys	Pro	Arg	Ala	Ile
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Val	Val	Asn	Ala	Glu	Arg	Gly	Tyr	Leu	Tyr	Phe	Thr	Asn	Met	Gln	Asp
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Val	Leu	Phe	Thr	Thr	Gly	Leu	Ile	Arg	Pro	Val	Ala	Leu	Val	Val	Asp
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Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn

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<222> (33739), (33749), (33758)
<223> Identity of nucleotide sequences at the above locations are unknown.

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<211> 25
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gcggggggcca acggggccctt cccgcacgag tatgtcagcg ggaccggca cgtgcccctc 420
aatttcatag ccccgccggt ttcccagcat ggcccccttca caggcatcgc atgcggaaag 480
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<220>
<223> Artificial Sequence is a primer.

<400> 636
agcgaggcca ccatccacag g 21

<210> 637
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<220>
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<400> 637
tcgctggtcg gcataatcaa t 21

<210> 638
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cacgtgattt agttggcct cgactaccct gaaggaatgg ctgtggactg gatgggcaag 240
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ttccggcagg tgcttgtgtg gagagacctt gacaacccca ggtctctggc tctggatcct 360
actaaaggtt acatctactg gactgagtgg ggtggcaagc caaggattgt gcgggccttc 420
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<212> RNA

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<223> Artificial Sequence is a Zmax1 oligonucleotide.

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26

<210> 641

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<223> Artificial Sequence is a Zmax1 oligonucleotide.

<400> 641

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26